

1 / 10

COPY OF PAPERS  
ORIGINALLY FILED

APPROVED BY	O.G. FIG.
DRAFTSMAN	CLASS SUBCLASS

Sequence

ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTTCICGATACCGAAACCACCGGTATGAACCAGATTGGT 75

\_\_\_\_\_mutD\_\_\_\_\_

M T A M S T A I T R Q I V L D T E T T G M N O I G

GCGCACTATGAAGGCCACAAGATCATTGAGATTGGTGCCGTIGAAGTGGTGAACCGTCGCCCTGACGGGCAATAAC 150

\_\_\_\_\_mutD\_\_\_\_\_

A H Y E G H K I I E I G A V E V V N R R L T G N N

TTCCATGTTTACTCAAAACCCGATCGGCTGGTGATCCGGAAGCCTTTGGCGTACATGGTATTGCCGATGAATTT 225

\_\_\_\_\_mutD\_\_\_\_\_

F H V Y L K P D R L V D P E A F G V H G I A D E F

TIGCTCGATAAGCCACGTTTGGCCGAAGTAGCCGATGAGTTCATGGACTATATTCCGGCGCGGAGTTGGTGATC 300

\_\_\_\_\_mutD\_\_\_\_\_

L L D K P T F A E V A D E F M D Y I R G A E L V I

CATAACGCAGCGTTCGATATCGGCITTTATGGACTACGAGTTTTCGTTGCTTAAGCGCGGATATCCGAAGACCAAT 375

\_\_\_\_\_mutD\_\_\_\_\_

H N A A F D I G F M D Y E F S L L K R D I P K T N

FIG.\_1A

2 / 10

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

ACTTICTGTAAGGTCACCGATAGCCTTGCGGTGGCGAGGAAATGTTTCCCGGTAAGCGCAACAGCCTCGATGCG 450

\_\_\_\_\_ mutD \_\_\_\_\_  
T F C K V T D S L A V A R K M F P G K R N S L D A

TIATGTGCTCGCTACGAAATAGATAACAGTAAACGAACGCTGCACGGGCATTACTCGATGCCAGATCCTTGCG 525

\_\_\_\_\_ mutD \_\_\_\_\_  
L C A R Y E I D N S K R T L H G A L L D A Q I L A

GAAGTTIATCTGGCGATGACCGGTGGTCAACGTCGATGGCTTTTTCGATGGAAGGAGAGACACACAGCAACAA 600

\_\_\_\_\_ mutD \_\_\_\_\_  
E V Y L A M T G G O T S M A F A M E G E T Q Q Q Q

GGTGAAGCAACAATTACGGCATTGTACGTCAGGCAAGTAAGTTACGCGTTGTTTTTTCGACAGATGAAGAGATT 675

\_\_\_\_\_ mutD \_\_\_\_\_  
G E A T I Q R I V R Q A S K L R V V F A T D E E I

GCAGCTCATGAAGCCCGTCTCGATCTGGTGCAGAGAAGCGGGAAGTTGCCTCTGGCGAGCATAA 741

\_\_\_\_\_ mutD \_\_\_\_\_  
A A H E A R L D L V O K K G G S C L W R A .

FIG..1B

3 / 10

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

10 20 30 40 50 60

10 ATGAGCTATCGTATGTTTGAATTAATCTGGTTCCAAATGTTGAACCTTCTTTTGGCCCGGGCGCC Eb\_429T.dna

10 ATGAGCTATCGTATGTTTGAATTAATCTGGTTCCAAATGTTGAACCTTCTTTTGGCCCGGGCGCC Eb\_GEBT.dna

70 80 90 100 110 120

70 GTTCTGTGTGTTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAATAAGCCCTGCTGGTGACC Eb\_429T.dna

70 GTTCTGTGTGTTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAATAAGCCCTGCTGGTGACC Eb\_GEBT.dna

130 140 150 160 170 180

130 GATAAGGGCCTGCGCGCCATTAAAGACGGTGCTGTCGATCAGACCGTGAAAGCACCTGAAA Eb\_429T.dna

130 GATAAGGGCCTGCGCGCCATTAAAGACGGTGCTGTCGATCAGACCGTGAAAGCACCTGAAA Eb\_GEBT.dna

190 200 210 220 230 240

190 GCCGCCGGTATTGAGGTGGTCAATTTTCGACGGGGGTCGAGCCGAAACCCGAAAGACACCAAC Eb\_429T.dna

190 GCCGCCGGTATTGAGGTGGTCAATTTTCGACGGGGGTCGAGCCGAAACCCGAAAGACACCAAC Eb\_GEBT.dna

250 260 270 280 290 300

250 GTGCTCGACGGCCTGGCCATGTTCCCGTAAAGAGCAGTGCGGACATGATAATCACCCGTCGGC Eb\_429T.dna

250 GTGCTCGACGGCCTGGCCATGTTCCCGTAAAGAGCAGTGCGGACATGATAATCACCCGTCGGC Eb\_GEBT.dna

FIG.--2A

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

	310	320	330	340	350	360	
310	G G C G G C A G C C C G C A C G A C T G C G G T A A A G G C A T T G G T A T T G C G G C C A C C C A C C C G G G T G A T						Eb_429T.dna
310	G G C G G C A G C C C G C T C G A C T G C G G T A A A G G C A T T G G T A T T G C G G C C A C C C A C C C G G G T G A T						Eb_GEBT.dna
	370	380	390	400	410	420	
370	C T G T A C A G C T A T G C C C G G T A T C G A A A C A C T C A C C A C C C G C T G C C G C C C C A T T A T T G C G G T C						Eb_429T.dna
370	C T G T A C A G C T A T G C C G G T A T C G A A A C A C A C T C A C C A C C C G C T G C C G C C C A T T A T T G C G G T C						Eb_GEBT.dna
	430	440	450	460	470	480	
430	A A C A C C A C C G C C G G G A C C G C C A G C G A A G T C A C C C G C C A C T G C G T G C T G A C T A A C A C C A A A						Eb_429T.dna
430	A A C A C C A C C G C C G G G A C C G C C A G C G A A G T C A C C C G C C A C T G C G T G C T G A C T A A C A C C A A A						Eb_GEBT.dna
	490	500	510	520	530	540	
490	A C C A A A G T A A A A T T T G T G A T T G T C A G C T G G C G C A A C C T G C C T T C C G T C T C C A T T A A C G A T						Eb_429T.dna
490	A C C A A A G T A A A A T T T G T G A T T G T C A G C T G G C G C A A C C T G C C T T C C G T C T C C A T T A A C G A T						Eb_GEBT.dna
	550	560	570	580	590	600	
550	C C G C T G C T G A T G A T C G G C A A G C C C G C C G G G C T G A C C G C C G C C A C C G G T A T G G A T G C C C T G						Eb_429T.dna
550	C C G C T G C T G A T G A T C G G C A A G C C C G C C G G G C T G A C C G C C G C C A C C G G T A T G G A T G C C C C T G						Eb_GEBT.dna

5/10

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

610	620	630	640	650	660	
610	A C C C A C G C G G T A G A G C C C T A T A T C T C C A A A G A C G C C A A C C C C G G T T A C C G A T G C C T C T G C T					Eb_429T.dna
610	A C C C A C G C G G T A G A G C C C T A T A T C T C C A A A G A C G C C A A C C C G G T T A C C G A T G C C T C T G C T					Eb_GEBT.dna
670	680	690	700	710	720	
670	A T T C A G G C C A T C A A A C T G A T T G C C A C C A A C T T G C G C C A G G C C G T C G C C C T G G G A C C A A C					Eb_429T.dna
670	A T T C A G G C C A T C A A A C T G A T T G C C A C C A A C T T G C G C C A G G C C G T C G C C C T G G G A C C A A C					Eb_GEBT.dna
730	740	750	760	770	780	
730	C T C A A A G C C C G T G A A A C A T G G C C C T G C G C C T C T C T G C T G G C C G G G A T G G C C T T T A A C A A C					Eb_429T.dna
730	C T C A A A G C C C G T G A A A C A T G G C C C T G C G C C T C T C T G C T G G C C G G G A T G G C C T T T A A C A A C					Eb_GEBT.dna
790	800	810	820	830	840	
790	G C C A A C C T G G G C T A T G T T C A C G C C C A T G G C T C A C C A G C T G G G C G G C C T G T A C G A C A T G G C C					Eb_429T.dna
790	G C C A A C C T G G G C T A T G T T C A C G C C C A T G G C T C A C C A G C T G G G C G G C C T G T A C G A C A T G G C C					Eb_GEBT.dna
850	860	870	880	890	900	
850	C A C G G G G T G G C G A A C G C G G G T C C T G C T G C C C C C A T G T C T G C C G C T A T A A C C T G A T T G C C A A C					Eb_429T.dna
850	C A C G G G G T G G C G A A C G C G G G T C C T G C T G C C C C C A T G T C T G C C G C T A T A A C C T G A T T G C C A A C					Eb_GEBT.dna

FIG..2C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 2D

910	920	930	940	950	960	
910	910	910	910	910	910	Eb_429T.dna
910	910	910	910	910	910	Eb_GEBT.dna
970	980	990	1000	1010	1020	
970	970	970	970	970	970	Eb_429T.dna
970	970	970	970	970	970	Eb_GEBT.dna
1030	1040	1050	1060	1070	1080	
1030	1030	1030	1030	1030	1030	Eb_429T.dna
1030	1030	1030	1030	1030	1030	Eb_GEBT.dna
1090	1100	1110	1120	1130	1140	
1090	1090	1090	1090	1090	1090	Eb_429T.dna
1090	1090	1090	1090	1090	1090	Eb_GEBT.dna
1150	1160	1170				
1150	1150	1150	1150	1150	1150	Eb_429T.dna
1150	1150	1150	1150	1150	1150	Eb_GEBT.dna

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG..2D

7 / 10

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

	10	40	70	100	
10	MSYRMFDYLVPNVNFPGPGAVSVVGQRCQLLGGKKALLVT				Eb_429T.dna
10	MSYRMFDYLVPNVNFPGPGAVSVVGQRCQLLGGKKALLVT				Eb_GEBT.dna
	130	160	190	220	
130	DKGLRAIKDGAVDQTVKHLKAAGIEVVIFDGVBNPKDTN				Eb_429T.dna
130	DKGLRAIKDGAVDQTVKHLKAAGIEVVIFDGVBNPKDTN				Eb_GEBT.dna
	250	280	310	340	
250	VLDGLAMFRKEQCMIITVGGGSPHDCGKGIGIAATHPGD				Eb_429T.dna
250	VLDGLAMFRKEQCMIITVGGGSPHDCGKGIGIAATHPGD				Eb_GEBT.dna
	370	400	430	460	
370	LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK				Eb_429T.dna
370	LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK				Eb_GEBT.dna
	490	520	550	580	
490	TKVKFVI VSWRNLP SVSINDP LLMIGKPA GLTAATGMDAL				Eb_429T.dna
490	TKVKFVI VSWRNLP SVSINDP LLMIGKPA GLTAATGMDAL				Eb_GEBT.dna

FIG.\_3A

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

[illegible]

	610	640	670	700	
610	THAVEAYISKDANPVTDA SAIQA I KLIATNL RQAV ALGTN				Eb_429T.dna
610	THAVEAYISKDANPVTDA SAIQA I KLIATNL RQAV ALGTN				Eb_GEBT.dna
	730	760	790	820	
730	LKARENMACASLLAGMAFN N ANLG YVHMAHQ LGGLYDMA				Eb_429T.dna
730	LKARENMACASLLAGMAFN N ANLG YVHMAHQ LGGLYDMA				Eb_GEBT.dna
	850	880	910	940	
850	HGVANA VLLPHVCRYN LIANPEKPADIA TFMGENTTG LST				Eb_429T.dna
850	HGVANA VLLPHVCRYN LIANPEKPADIA TFMGENTTG LST				Eb_GEBT.dna
	970	1000	1030	1060	
970	MDAAELAISAIARLSKDVGIPQH LRELGVKEADFPYMAEM				Eb_429T.dna
970	MDAAELAISAIARLSKDVGIPQH LRELGVKEADFPYMAEM				Eb_GEBT.dna
	1090	1120	1150		
1090	ALKDGNAFSNPRKGNEKEIADI PRQAP				Eb_429T.dna
1090	ALKDGNAFSNPRKGNEKEIADI PRQAP				Eb_GEBT.dna

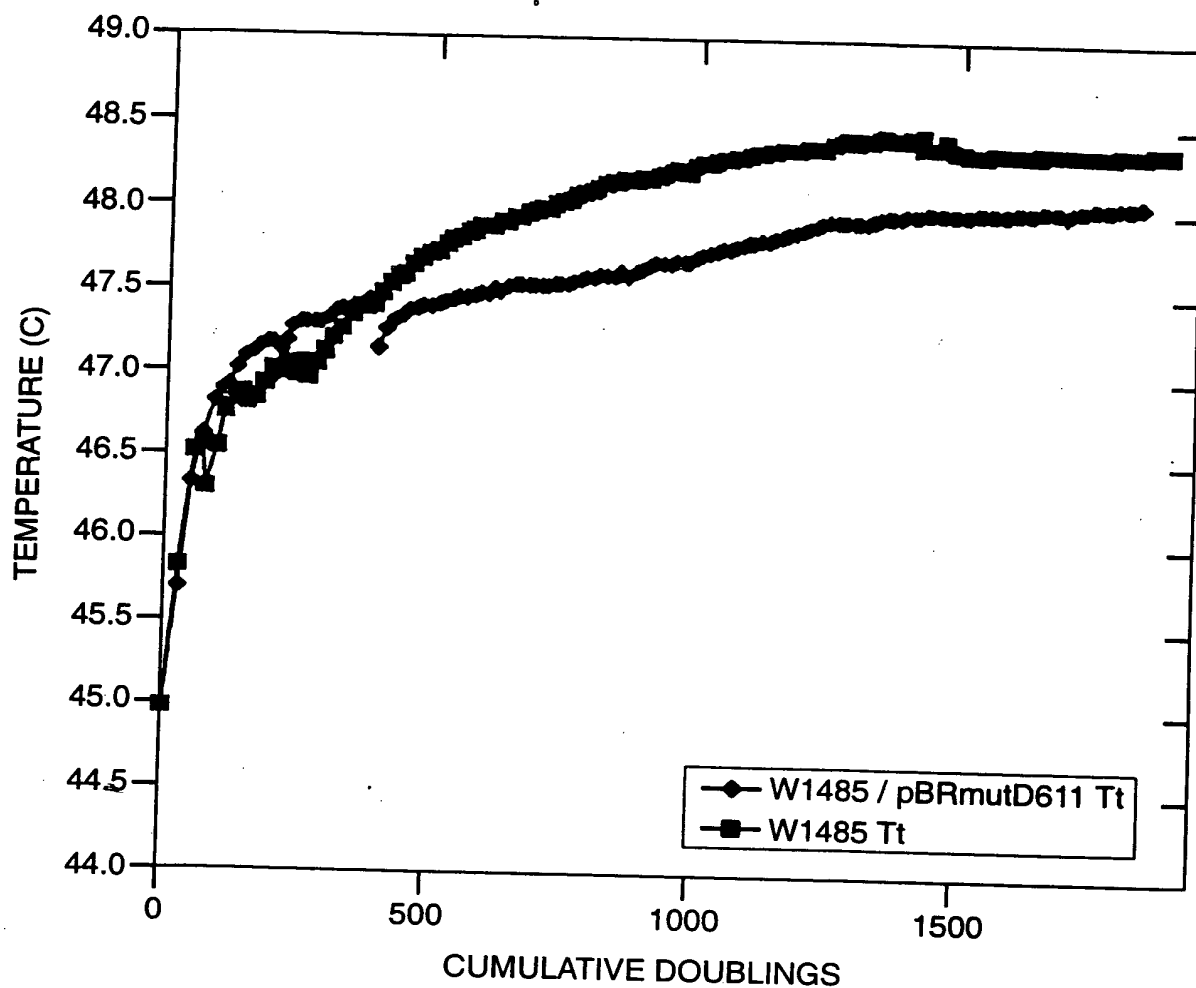
Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

**FIG. 3B**



9 / 10

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY		
DRAFTSMAN		



**FIG.\_4**

10 / 10

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY		
DRAFTSMAN		

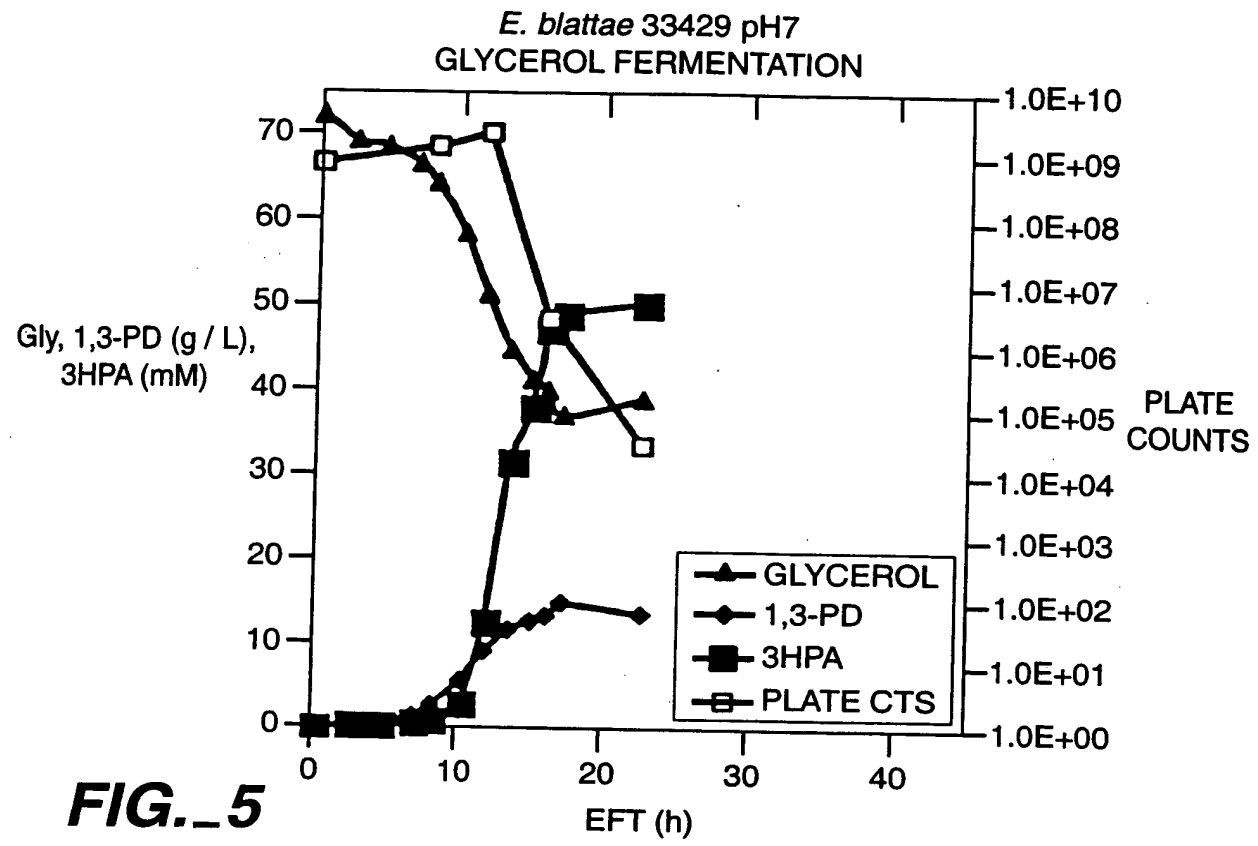


FIG.\_5

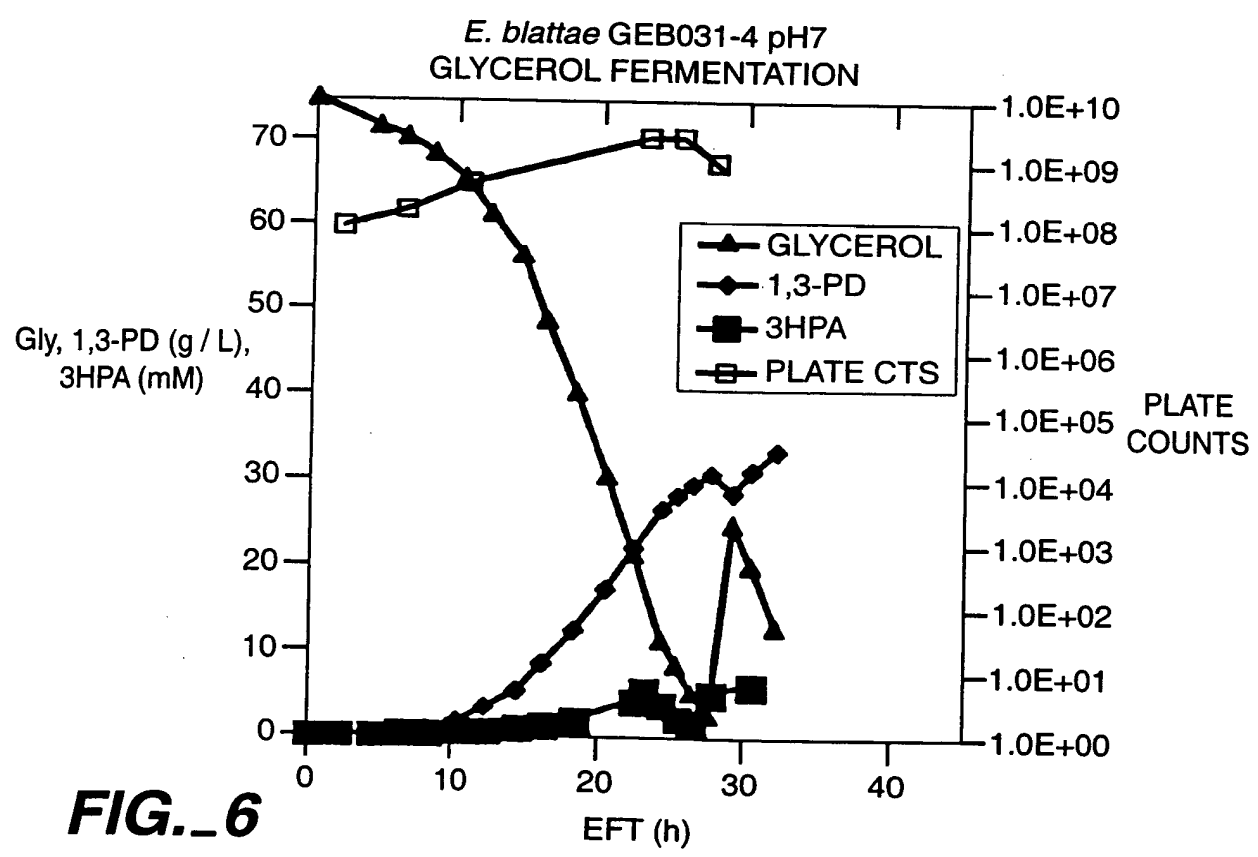


FIG.\_6